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SEQUENCE LISTING

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Umemura, Mariko  
Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT  
INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10/536,935  
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<150> PCT/JP03/14909  
<151> 2003-11-21

<150> JP 2002-339418  
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gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg 144  
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aaa aat tcc aac ctt atg cct ggc att tcc agc gtg caa tac ata 192  
Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile  
50 55 60

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65 70 75 80

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Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Pro Cys

85	90	95	
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gaa aaa aag ccgttatattactgcgttatcggtggatgttttattctg Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Met Leu Ile Leu 130	135	140	432
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ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val 165	170	175	528
gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu 180	185	190	576
aaa aac cta agc ttg aag agt aaa ccc agc ttc tta aaa aat gca ttt Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe 195	200	205	624
aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg 210	215	220	672
ttg ttt ttgttatatatca gaa tat caa gaa cat gtc aca gaa tat Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr 225	230	235	720
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gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe 305	310	315	960
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465 470 475 480	
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Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile  
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Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys  
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Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Lys Pro Ser  
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Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu  
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Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu  
 130 135 140

Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg  
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Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val  
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 180 185 190

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe  
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Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg  
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Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr  
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Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val  
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 260 265 270

Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp  
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Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser  
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Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe  
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 340 345 350

Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser  
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 Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro  
 385 390 395 400  
 Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr  
 405 410 415  
 Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val  
 420 425 430  
 Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu  
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 450 455 460  
 Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser  
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Thr Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
    20          25          30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
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gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
    50          55          60

att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240
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    65          70          75          80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
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115	120	125	
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Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu			
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gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa		528	
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Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala			
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Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser			
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Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn			
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405	410	415	
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435	440	445	
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Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln			
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180		185	190
Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val			
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Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala			
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Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val			
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325		330	335
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Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu			
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Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser			
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Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn			

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85               90               95

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Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu  
100              105              110

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ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val 195	200	205	624
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cca cgc ttc ata ata gga att ggt atc tca att ggt tat gag gta gcg Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala 260	265	270	816
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gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser 370 375 380	1152
aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn 385 390 395 400	1200
gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly 405 410 415	1248
aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe 420 425 430	1296
atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile 435 440 445	1344
aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly 450 455 460	1392
tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys 465 470 475 480	1440
atc tac atc aag ctt tag Ile Tyr Ile Lys Leu 485	1458

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<211> 485  
<212> PRT  
<213> Candida albicans

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Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu 20 25 30
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu 35 40 45
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser 50 55 60
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val 65 70 75 80
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro 85 90 95
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu 100 105 110

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu  
 115 120 125  
 Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro  
 130 135 140  
 Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu  
 145 150 155 160  
 Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln  
 165 170 175  
 Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr  
 180 185 190  
 Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val  
 195 200 205  
 Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu  
 210 215 220  
 His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly  
 225 230 235 240  
 Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val  
 245 250 255  
 Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala  
 260 265 270  
 Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg  
 275 280 285  
 Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile  
 290 295 300  
 Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val  
 305 310 315 320  
 Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile  
 325 330 335  
 Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser  
 340 345 350  
 Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu  
 355 360 365  
 Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser  
 370 375 380  
 Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn  
 385 390 395 400  
 Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly  
 405 410 415  
 Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe  
 420 425 430  
 Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

Asn	Thr	Leu	Glu	Thr	Ser	Asn	Lys	Met	Ala	Val	Ile	Ile	Leu	Ile	Gly
450						455					460				

Tyr	Ser	Leu	Thr	Trp	Thr	Leu	Leu	Ala	Leu	Tyr	Leu	Asp	Lys	Arg	Lys
465					470					475			480		

Ile	Tyr	Ile	Lys	Leu
		485		

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<212> DNA  
<213> Schizosaccharomyces pombe

<220>  
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Met	Ser	Tyr	Lys	Leu	Glu	Lys	Glu	Ala	Phe	Val	Ser	Asn	Leu	Thr	Gly
1			5						10				15		
tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc										96					
Ser	Ser	Ser	Ile	Glu	Thr	Cys	Gly	Leu	Leu	Leu	Ile	Gly	Ile	Ala	Cys
20				25							30				
aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg										144					
Asn	Val	Leu	Trp	Val	Asn	Met	Thr	Ala	Arg	Asn	Ile	Leu	Pro	Lys	Gly
35				40						45					
aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta										192					
Asn	Leu	Gly	Phe	Leu	Val	Glu	Phe	Phe	Ile	Phe	Cys	Leu	Ile	Pro	Leu
50				55					60						
ttt gtc att tac gtt tca tcg aaa gtt ggc gtt ttc act ctt tgc ata										240					
Phe	Val	Ile	Tyr	Val	Ser	Ser	Lys	Val	Gly	Val	Phe	Thr	Leu	Cys	Ile
65				70					75			80			
gcc tct ttt ttg cct tcc gtc ctt cat gtt ata agt cca att aat										288					
Ala	Ser	Phe	Leu	Pro	Ser	Phe	Val	Leu	His	Val	Ile	Ser	Pro	Ile	Asn
85					90					95					
tgg gat gtg ctg aga aga aaa cct ggt tgt ctt act aaa aaa aat										336					
Trp	Asp	Val	Leu	Arg	Arg	Lys	Pro	Gly	Cys	Cys	Leu	Thr	Lys	Lys	Asn
100				105						110					
gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct										384					
Glu	Asn	Thr	Phe	Asp	Arg	Arg	Ile	Ala	Gly	Val	Thr	Phe	Tyr	Arg	Ser
115				120						125					
caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc										432					
Gln	Met	Met	Leu	Val	Thr	Val	Thr	Cys	Ile	Leu	Ala	Val	Asp	Phe	Thr
130				135						140					
ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg										480					
Leu	Phe	Pro	Arg	Arg	Tyr	Ala	Lys	Val	Glu	Thr	Trp	Gly	Thr	Ser	Leu

145	150	155	160	
atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg gct Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala				528
165	170	175		
gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg Gly Arg Lys Asn Asp Ile Lys Pro Asn Ala Phe Lys Asn Val Leu				576
180	185	190		
tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu				624
195	200	205		
acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His				672
210	215	220		
tgg aac ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe				720
225	230	235	240	
ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe				768
245	250	255		
att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys				816
260	265	270		
tgg gca cta tcc gcc ccc aga aca aat att ttg gct cag aat aga gag Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu				864
275	280	285		
ggg att gct tct ctt ccc gga tac att gct att tac ttt tat gga atg Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met				912
290	295	300		
tat acc ggt agt gta gtt ttg gct gat cga cct cta atg tat act aga Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg				960
305	310	315	320	
gct gag tcg tgg aag cgc ttt caa cgt cta tta ttc ccg cta tgc att Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile				1008
325	330	335		
ttg tta gtg ttg tat ctt gtg tct aac ttt ttg tca gtt ggt gtt tct Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser				1056
340	345	350		
cgc cga ctt gct aat acg cct tat gtt gcg aat gtt gcc ttt atc aat Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn				1104
355	360	365		
atg ttt ttt ctt act ata tac ata ctt att gat gcc tat tta ttc cca Met Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro				1152
370	375	380		
tct tct gtg cca tat gga agt cgc gtc ccc aaa ctg ctt gaa gat gcc Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala				1200
385	390	395	400	

aat aat aat ggc ttg ttg gtg ttt ttg att gct aac gtt tta aca gga 1248  
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly  
405 410 415

gta gtt aat tta tcg ttc gac acc ctt cat tct agc aat gca aaa ggc 1296  
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly  
420 425 430

ttg aca atc atg act atg tat ctt ttt att att tgc tat atg gca cat 1344  
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His  
435 440 445

tgg ctt gct caa cac gga att cgt ttt cgc ctt tag 1380  
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu  
450 455

<210> 8  
<211> 459  
<212> PRT  
<213> Schizosaccharomyces pombe

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Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys  
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Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly  
35 40 45

Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu  
50 55 60

Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile  
65 70 75 80

Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn  
85 90 95

Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn  
100 105 110

Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser  
115 120 125

Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr  
130 135 140

Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu  
145 150 155 160

Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala  
165 170 175

Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu  
180 185 190

Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu

195	200	205
Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His		
210	215	220
Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe		
225	230	235
Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe		
245	250	255
Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys		
260	265	270
Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu		
275	280	285
Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met		
290	295	300
Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg		
305	310	315
320		
Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile		
325	330	335
Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser		
340	345	350
Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn		
355	360	365
Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro		
370	375	380
Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala		
385	390	400
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly		
405	410	415
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly		
420	425	430
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His		
435	440	445
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu		
450	455	

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 <211> 1576  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
 <221> CDS  
 <222> (31)..(1536)

<400> 9

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aaa gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile 10 15 20	102
aac gcc gtc acc ttg gtt gct tcg gta tcc gtt ttt ctg tgg tca att Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile 25 30 35 40	150
cta caa tct cgc cta tcc ttt ttc aca ccc tac agc gcc gct gcc ctt Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr Ser Ala Ala Ala Leu 45 50 55	198
ctc gtt gat ttc ctg ctc aat gta cta gct atc ttg ttc gca acc act Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr 60 65 70	246
tta tac tct tcg gcg cct ctt ctc aat ctc ctt cta ata tct ccc Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu Leu Leu Ile Ser Pro 75 80 85	294
gct ctg ctg ata ctc ctc tct acg aaa cgt cct cg <sup>g</sup> acc ccc gtc aaa Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys 90 95 100	342
g <sup>c</sup> g aaa cct cct cgc cag tcc gct aga gct ggg aaa gat gac tcg aaa Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys 105 110 115 120	390
cat g <sup>c</sup> g aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr 125 130 135	438
aca tat cgc gcc gcc atg atg gtt atc acg tgc atc gct atc ttg gct Thr Tyr Arg Ala Ala Met Val Ile Thr Cys Ile Ala Ile Leu Ala 140 145 150	486
gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp 155 160 165	534
ggt aca tca ctc atg gat ctg ggc gtt gga tcg ttt gtc ttt tcg ggc Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly 170 175 180	582
gga gta gta tcc gct cgc tca cta ctc aag agc agg acc aat ggc tct Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser Arg Thr Asn Gly Ser 185 190 195 200	630
aaa agg ttg cct ctt gcc aag agg ttg att g <sup>c</sup> g tcg acg cga cac tct Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser 205 210 215	678
att cct ctg ctc gtc ctc ggc ctg att cgg cta tac agc gtc aaa ggc Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly 220 225 230	726
ttg gac tat g <sup>c</sup> g gag cac gtc acc gag tac ggc gta cat tgg aac ttc	774

Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe			
235	240	245	
ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg gag gac gtc ttc gac gcc			
Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val Glu Val Phe Asp Ala			
250	255	260	822
ttg gct acg atc att ccg tca tac gag gtt ctc tcc gtg ggg atc gcc			
Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu Ser Val Gly Ile Ala			
265	270	275	280
gtc ttg tat caa gtt gcc cta gag tca aca gac ttg aaa agc tac atc			
Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp Leu Lys Ser Tyr Ile			
285	290	295	918
ctc gtc tcc cct cgt ggg cca agc tta ctg tcc aag aat cgt gaa ggc			
Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser Lys Asn Arg Glu Gly			
300	305	310	966
gtc ttc tcc ttc tca ggt tat ctc gcg att ttt ctt gct ggt cgt gcg			
Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe Leu Ala Gly Arg Ala			
315	320	325	1014
atc ggc att cgg ata atc cct cgc gga act tct ttc tca aga agc cca			
Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser Phe Ser Arg Ser Pro			
330	335	340	1062
gaa cag gcc agg aga cgg gtc ctg atc agc ctt ggc gtg caa gcg tta			
Glu Gln Ala Arg Arg Arg Val Leu Ile Ser Leu Gly Val Gln Ala Leu			
345	350	355	360
gtg tgg acc act ctt ttt gtg ttg aac tcc act tat gcg atg gga tac			
Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr Tyr Ala Met Gly Tyr			
365	370	375	1158
gga gct aat atc cct gtc tcc cgc cgc ctc gct aac atg ccc tat gtc			
Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala Asn Met Pro Tyr Val			
380	385	390	1206
ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg ttt gtg ttc tgc ctg			
Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu Phe Val Phe Cys Leu			
395	400	405	1254
atc gaa aca ctc tgc ttt cct gca gtt cat cgg aca acg act caa gag			
Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg Thr Thr Gln Glu			
410	415	420	1302
agc gaa tct gag cga gtc gat ttt gct acg agc cga atc atg tcg gcc			
Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser Arg Ile Met Ser Ala			
425	430	435	440
ttc aat aag aac agt ctc gcg atc ttt ctt ttg gcc aat ctt ctg act			
Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu Ala Asn Leu Leu Thr			
445	450	455	1398
gga gct gtg aat ctg agc atc tcc aca att gat gct aat aca gcg cag			
Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp Ala Asn Thr Ala Gln			
460	465	470	1446
gcc atc gct gtt ctc att gga tat tca tcc att atc aca ggg gtt gct			
Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile Ile Thr Gly Val Ala			
494			1494

475	480	485	
cta gca ttg cat cat gcc aat atc aaa gta ctt cct ttc tag			
Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe			
490	495	500	
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Ala Gly Gly Ser Ile Leu Glu Ile Asn Ala Val Thr Leu Val Ala Ser			
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Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe			
35	40	45	
Thr Pro Tyr Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val			
50	55	60	
Leu Ala Ile Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu			
65	70	75	80
Leu Asn Leu Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr			
85	90	95	
Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala			
100	105	110	
Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser			
115	120	125	
Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val			
130	135	140	
Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg			
145	150	155	160
Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly			
165	170	175	
Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu			
180	185	190	
Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg			
195	200	205	
Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu			
210	215	220	
Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr			
225	230	235	240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro  
 245 250 255  
 Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr  
 260 265 270  
 Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu  
 275 280 285  
 Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser  
 290 295 300  
 Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu  
 305 310 315 320  
 Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg  
 325 330 335  
 Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu  
 340 345 350  
 Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu  
 355 360 365  
 Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg  
 370 375 380  
 Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr  
 385 390 395 400  
 Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala  
 405 410 415  
 Val His Arg Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe  
 420 425 430  
 Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile  
 435 440 445  
 Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser  
 450 455 460  
 Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr  
 465 470 475 480  
 Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile  
 485 490 495  
 Lys Val Leu Pro Phe  
 500

<210> 11  
 <211> 1648  
 <212> DNA  
 <213> Aspergillus fumigatus

<220>  
 <221> intron  
 <222> (122)..(198)

<220>  
<221> CDS  
<222> (26)..(121)

<220>  
<221> CDS  
<222> (199)..(1608)

<400> 11

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			1					5								
gag	gcc	ttt	gtc	tca	ggg	ctt	gca	gga	gga	agc	atc	ctg	gaa	atc	aac	100
Glu	Ala	Phe	Val	Ser	Gly	Leu	Ala	Gly	Gly	Ser	Ile	Leu	Glu	Ile	Asn	
10		15				20					25					
gcc	gtc	acc	ttg	gtt	gct	tcg	gttcgtgtta	ctatcttatt	gtggctactt						151	
Ala	Val	Thr	Leu	Val	Ala	Ser										
			30													
cgcctacatt	gtttctcgac	taaccgagtc	tctttgcgt	aatcag	gta	tcc	gtt							207		
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Phe	Leu	Trp	Ser	Ile	Leu	Gln	Ser	Arg	Leu	Ser	Phe	Phe	Thr	Pro	Tyr	
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agc	gcc	gct	gcc	ctt	ctc	gtt	gat	ttc	ctg	ctc	aat	gta	cta	gct	atc	303
Ser	Ala	Ala	Leu	Leu	Val	Asp	Phe	Leu	Leu	Asn	Val	Leu	Ala	Ile		
55		60				65										
ttg	tcc	gca	acc	act	tta	tac	tct	tcg	gct	cct	ttt	ctc	aat	ctc		351
Leu	Phe	Ala	Thr	Thr	Leu	Tyr	Ser	Ser	Ala	Pro	Leu	Leu	Asn	Leu		
70		75				80										
ctt	cta	ata	tct	ccc	gct	ctg	ctg	ata	ctc	ctc	tct	acg	aaa	cgt	cct	399
Leu	Leu	Ile	Ser	Pro	Ala	Leu	Leu	Ile	Leu	Leu	Ser	Thr	Lys	Arg	Pro	
85		90				95										
cgg	acc	ccc	gtc	aaa	gct	aaa	cct	cct	cgc	cag	tcc	gct	aga	gct	ggg	447
Arg	Thr	Pro	Val	Lys	Ala	Lys	Pro	Pro	Arg	Gln	Ser	Ala	Arg	Ala	Gly	
100		105				110				115						
aaa	gat	gac	tcg	aaa	cat	gct	aca	gcc	ttg	cca	gag	tct	cta	ccc	att	495
Lys	Asp	Asp	Ser	Lys	His	Ala	Thr	Ala	Leu	Pro	Glu	Ser	Leu	Pro	Ile	
120		125				130										
cat	cca	ttt	ctc	acg	aca	tat	cgc	gcc	atg	atg	gtt	atc	acg	tgc		543
His	Pro	Phe	Leu	Thr	Thr	Tyr	Arg	Ala	Ala	Met	Met	Val	Ile	Thr	Cys	
135		140				145										
atc	gct	atc	ttg	gct	gtg	gat	ttt	cgc	att	ttt	cct	cgc	cga	ttc	gcc	591
Ile	Ala	Ile	Leu	Ala	Val	Asp	Phe	Arg	Ile	Phe	Pro	Arg	Arg	Phe	Ala	
150		155				160										
aag	gta	gaa	aac	tgg	ggt	aca	tca	ctc	atg	gat	ctg	ggc	gtt	gga	tcg	639
Lys	Val	Glu	Asn	Trp	Gly	Thr	Ser	Leu	Met	Asp	Leu	Gly	Val	Gly	Ser	
165		170				175										

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agg acc aat ggc tct aaa agg ttg cct ctt gcc aag agg ttg att gcg Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala 200 205 210	735
tcg acg cga cac tct att cct ctg ctc gtc ctc ggc ctg att cgg cta Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu 215 220 225	783
tac agc gtc aaa ggc ttg gac tat gcg gag cac gtc acc gag tac ggc Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly 230 235 240	831
gta cat tgg aac ttc ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg Val His Trp Asn Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val 245 250 255	879
gag gtc ttc gac gcc ttg gct acg atc att ccg tca tac gag gtt ctc Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu 260 265 270 275	927
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ggc gtg caa gcg tta gtg tgg acc act ctt ttt gtg ttg aac tcc act Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr 360 365 370	1215
tat gcg atg gga tac gga gct aat atc cct gtc tcc cgc cgc ctc gct Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala 375 380 385	1263
aac atg ccc tat gtc ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu 390 395 400	1311
ttt gtg ttc tgc ctg atc gaa aca ctc tgc ttt cct gca gtt cat cgg Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg 405 410 415	1359
aca acg actcaa gag agc gaa tct gag cga gtc gat ttt gct acg agc	1407

Thr	Thr	Thr	Gln	Glu	Ser	Glu	Ser	Glu	Arg	Val	Asp	Phe	Ala	Thr	Ser	
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Arg	Ile	Met	Ser	Ala	Phe	Asn	Lys	Asn	Ser	Leu	Ala	Ile	Phe	Leu	Leu	
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gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat															1503	
Ala	Asn	Leu	Leu	Thr	Gly	Ala	Val	Asn	Leu	Ser	Ile	Ser	Thr	Ile	Asp	
					455				460					465		
gct aat aca gca cag gcc atc gct gtt ctc att gga tat tca tcc att															1551	
Ala	Asn	Thr	Ala	Gln	Ala	Ile	Ala	Val	Leu	Ile	Gly	Tyr	Ser	Ser	Ile	
					470				475					480		
atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt															1599	
Ile	Thr	Gly	Val	Ala	Leu	Ala	Leu	His	His	Ala	Asn	Ile	Lys	Val	Leu	
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Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu																
25 30																
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ggggttctgt catttggaga cgcttattaa ttggatcgc ag gcg aca tat gct																
Ala Thr Tyr Ala																
35																
210																

ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn	40	45	50	258
tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser	55	60	65	306
act tcg cct ctc gta ttt acc tct ttt ttg tcc att att tcc ctc gct Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala	70	75	80	354
ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt tcg ccc gaa Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu	85	90	95	402
aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat gag gaa cca Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro	100	105	110	115
gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys	120	125	130	498
ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta tta tct ccc Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu Leu Ser Pro	135	140	145	546
gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca gct tca gga Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ala Ser Gly	150	155	160	594
cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg agg tcg cta His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg Arg Ser Leu	165	170	175	642
tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac tcc aag gtc Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp Ser Lys Val	180	185	190	195
aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct agg gca acg Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser Arg Ala Thr	200	205	210	738
aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt ttg aca gtg Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe Leu Thr Val	215	220	225	786
tac cga gcg cac atg atg ctc atg act gtt atc tgc atc ttg gcg gta Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile Leu Ala Val	230	235	240	834
gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa gat ttt ggt Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu Asp Phe Gly	245	250	255	882
act agt ctg gtaagcttc cttagccat ggccaggc tcaccgctct Thr Ser Leu				931
				260

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ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act cct acg ccc Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr Pro Thr Pro 280 285 290	1029
tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc ccg tcc ccg Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr Pro Ser Pro 295 300 305	1077
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ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg cag tgg ctt Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr Gln Trp Leu 360 365 370	1269
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agt tta cca cca aga aga gag agg gtc gtg tca gaa aca aat gaa gag Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr Asn Glu Glu 440 445 450	1509
cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg att atg gag His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu Ile Met Glu 455 460 465	1557
ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga ggc tgg att Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly Gly Trp Ile 470 475 480	1605
tgg gcc ggc ggg gag gta tcc agg cgt tta gtaagtggac atctttggta Trp Ala Gly Gly Glu Val Ser Arg Arg Leu 485 490	1655
atattgtacc tatactaatac cctgcataaaa g gcc aac gct cct tat gta ttt	1707

	Ala Asn Ala Pro Tyr Val Phe	
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Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly Tyr Leu Leu		
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acc cac att att cca tct ccc acc tct tcc caa aca tca cca tcg atc		1803
Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr Ser Pro Ser Ile		
520	525	530
tta gtg cct ccc ttg ctc gac gct atg aat aaa aac ggt ctc gcg ata		1851
Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn Gly Leu Ala Ile		
535	540	545
ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat gtg agc atg aag		1899
Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn Val Ser Met Lys		
550	555	560
aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg tta atg ttg tat		1947
Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val Leu Met Leu Tyr		
565	570	575
acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa gga cgg agg atc		1995
Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys Gly Arg Arg Ile		
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aag ata tagttaaagt gtttaccatg caggatactg agtatctcggttca		2045
Lys Ile		

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ggt gct tct atc tgg agt atc aac gct gtc agc ctg gtc gca ctg gcg		96
Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala		
20	25	30
aca tat gct ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc		144
Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu		
35	40	45
ctg aac aac tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc		192
Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr		
50	55	60
atc ttc tca act tcg cct ctc gta ttt acc tct ttt ttg tcc att att		240
Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile		
65	70	75
		80

tcc ctc gct ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser	288
85 90 95	
tcg ccc gaa aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp	336
100 105 110	
gag gaa cca gcg gaa cct gct tct gca gct gga tct gca gca gtc tca Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser	384
115 120 125	
cca gta aag ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu	432
130 135 140	
tta tct ccc gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser	480
145 150 155 160	
gct tca gga cat gaa gac cct ttg ggg att atg ggc gtt aac aga cg Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg	528
165 170 175	
agg tcg cta tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp	576
180 185 190	
tcc aag gtc aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser	624
195 200 205	
agg gca acg aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe	672
210 215 220	
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225 230 235 240	
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245 250 255	
gat ttt ggt act agt ctg atg gac gtg ggt gtc ggg tca ttc gtc ttt Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe	816
260 265 270	
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275 280 285	
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290 295 300	
ccg tcc ccg tt <sup>c</sup> act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc	960

Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro			
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atc ctc gtc ctc ggc ttt ata cgg ttg att atg gtc aag gga tct gat			1008
Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp			
325	330	335	
tat cct gag cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc			1056
Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe			
340	345	350	
acc ctc gca ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg			1104
Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr			
355	360	365	
cag tgg ctt cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat			1152
Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His			
370	375	380	
cag ctg tgg tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc			1200
Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly			
385	390	395	400
cgg tca ggt atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct			1248
Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro			
405	410	415	
ggt tat ctt tcc ata ttt ttg atc ggc ttg tct att gga gat cat gtt			1296
Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val			
420	425	430	
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Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr			
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485	490	495	
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Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly			
500	505	510	
tac ctc ctc ctt acc cac att att cca tct ccc acc tct tcc caa aca			1584
Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr			
515	520	525	
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Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn			
530	535	540	
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Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn			

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Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr 50 55 60				
Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile 65 70 75 80				
Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser 85 90 95				
Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp 100 105 110				
Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser 115 120 125				
Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu 130 135 140				
Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser 145 150 155 160				
Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg 165 170 175				
Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp 180 185 190				
Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser 195 200 205				
Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe				

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225	230	235
Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu		
245	250	255
Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe		
260	265	270
Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr		
275	280	285
Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr		
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Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro		
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Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp		
325	330	335
Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe		
340	345	350
Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr		
355	360	365
Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His		
370	375	380
Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly		
385	390	395
Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro		
405	410	415
Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val		
420	425	430
Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr		
435	440	445
Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu		
450	455	460
Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly		
465	470	475
Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala		
485	490	495
Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly		
500	505	510
Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr		
515	520	525
Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn		

530

535

540

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn  
545 550 555 560

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val  
565 570 575

Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys  
580 585 590

Gly Arg Arg Ile Lys Ile  
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<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

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35

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<211> 34

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

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39

<210> 17

<211> 60

<212> DNA

<213> *Saccharomyces cerevisiae*

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60

<210> 18

<211> 60

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 18

ttatagctta atgaatattc ttttctata caagaaaacc gaattcgagc tcgtttaaac

60